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OM protein - protein search, using sw model

Run on: January 3, 2003, 13:01:31 ; Search time 3.69565 Seconds  
(without alignments)  
112.230 Million cell updates/sec

Title: US-09-801-784a-36

Perfect score: 50  
Sequence: 1 PSAAVLTSP 10

Scoring table: BL0SUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	88.0	171	1	FMS1_ECOLI
2	40	80.0	170	1	PMO1_ECOLI
3	36	72.0	234	1	POLN_RHDV3
4	36	72.0	326	1	MTC2_CHVP1
5	36	72.0	377	1	VMAT_PI2HT
6	36	72.0	2344	1	POLN_RHDV
7	35	70.0	374	1	ADH7_HUMAN
8	35	70.0	374	1	ADH7_MOUSE
9	35	70.0	486	1	RTG3_YEAST
10	35	70.0	845	1	KRUH_DROME
11	35	70.0	963	1	CHS2_YEAST
12	35	70.0	2663	1	LRBA_HUMAN
13	34	68.0	540	1	ANPC_HUMAN
14	34	68.0	736	1	DVU2_MOUSE
15	34	68.0	943	1	BLI4_CAEEL
16	34	68.0	2016	1	CINS_HUMAN
17	33.5	67.0	291	1	GYBP_SULAC
18	33	66.0	314	1	GBLP_SCHPO
19	33	66.0	369	1	VMAT_LPMV
20	33	66.0	375	1	ADHA_UFOHA
21	33	66.0	382	1	VMAT_SV41
22	33	66.0	438	1	EFIA_DESMO
23	33	66.0	547	1	FIB1_ADE40
24	33	66.0	561	1	ATKA_ANASU
25	33	66.0	664	1	PTSA_ANASU
26	33	66.0	680	1	DAP1_HUMAN
27	33	66.0	919	1	PWP2_HUMAN
28	33	66.0	1274	1	SRP3_BACSU
29	33	66.0	1301	1	AKX1_HUMAN
30	32	64.0	123	1	SDIS_NCCSI
31	32	64.0	169	1	CU21_LOCM1
32	32	64.0	252	1	BTG3_MOUSE
33	32	64.0	307	1	YL72_ARCFU

34	32	64.0	326	1	Y800_PYPAB	Q9U2E8 PYROCOCUS
35	32	64.0	384	1	SDC3_HUMAN	O75056 Homo sapien
36	32	64.0	428	1	EF1A_PYPAB	Q9V0V7 PYROCOCUS
37	32	64.0	428	1	EF1A_PYPAB	O59153 PYROCOCUS
38	32	64.0	430	1	EF1A_PYPAB	P26751 PYROCOCUS
39	32	64.0	437	1	EF1A_AERPE	Q9YAV0 aetopyrum p
40	32	64.0	787	1	DPOL_HPBDC	P30028 duck hepati
41	32	64.0	788	1	DPOL_HPBDC	P17192 duck hepati
42	32	64.0	788	1	DPOL_HPBDC	P17193 duck hepati
43	31	62.0	85	1	HPIS_THIRO	P00261 thlocapsa r
44	31	62.0	194	1	VE6A_SCHPO	O14256 schizosach
45	31	62.0	274	1	VGLE_HSV2	P13289 herpes simp

#### ALIGNMENTS

RESULT 1  
FMS1\_ECOLI  
ID FMS1\_ECOLI STANDARD; PRT; 171 AA.  
AC P25730;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE CSI fimbrial subunit A precursor (CSI pilin).  
GN CSOA OR COOA.  
OS Escherichia coli.  
OC Plasmid pDEP23, and Plasmid pF605.  
OC Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RX MEDLINE=91357443; PubMed=1679404;  
RA Jordan B.J.A.M., van Vliet A.H.M., Willems G.A.,  
van der Zeijst B.A.M., Gaastera W.;  
RT "Analysis of the first two genes of the CSI fimbrial operon in human  
enterotoxigenic Escherichia coli of serotype O139:H28."  
RL FEMS Microbiol. Lett. 64:265-270(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O6:H16; PLASMID=pDEP23;  
RX MEDLINE=91034170; PubMed=1977705;  
RA Perez-Casal J., Swartley J.S., Scott J.R.;  
RT "Gene encoding the major subunit of CSI pilin of human enterotoxigenic  
Escherichia coli."  
RL Infect. Immun. 58:3594-3600(1990).  
RN [3]  
RP SEQUENCE OF 24-42.  
RC STRAIN=60R75;  
RX MEDLINE=90036735; PubMed=2572583;  
RA Hall R.H., Kaneval D.R. Jr., Collins J.H., Theibert J.L.,  
Levine M.W.;  
RT "Purification and analysis of colonization factor antigen I, coli  
surface antigen 1, and coli surface antigen 3 fimbriae from  
enterotoxigenic Escherichia coli."  
RL J. Bacteriol. 171:6372-6374(1989).  
RN [4]  
RP FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING  
FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5  
MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO  
COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.  
CC -!- INDUCTION: CSI FIMBRIAE ARE ONLY EXPRESSED IN THE PRESENCE OF THE  
POSITIVE REGULATOR RNS.  
CC -!- SIMILARITY: TO THE CFA/I FIMBRIAL SUBUNIT B (CFAB).  
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CC -----
DR EMBL; X62879; CAA44673.1; -
DR EMBL; M58550; AAA23596.1; -
DR PIR; A41467; A41467.
DR PIR; S19003; S19003.
KW Fimbrin; Signal; Plasmid.
FT SIGNAL 1 23
FT CHAIN 24 171 CS1 FIMBRIAL SUBUNIT A.
FT CONFLICT 28 28 I -> E (IN REF. 3).
SQ SEQUENCE 171 AA; 17542 MW; 46E70EE7053DBE13 CRC64;

Query Match 88.0%; Score 44; DB 1; Length 171;
Best Local Similarity 80.0%; Pred. No. 0.09;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSVALTYSP 10
Db 49 PSVALTYSP 58

RESULT 2
FMCI ECOLI
ID FMC1 ECOLI STANDARD; PRT; 170 AA.
AC P02971;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CFA/I fimbrial subunit B precursor (Colonization factor antigen I subunit B) (CFA/I pilin) (CFA/I antigen).
EN CFAB.
GN Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89173309; PubMed=2564374;
RA Karjalainen T.K., Evans D.G., So M., Lee C.-H.;
RT "Molecular cloning and nucleotide sequence of the colonization factor antigen I gene of Escherichia coli.";
RL Infect. Immun. 57:1126-1130(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89330163; PubMed=2569152;
RA Hamers A.M., Pel H.J., Willshaw G.A., Kusters J.G.,
RA van der Zeijst B.A.M., Gaastra W.;
RT "The nucleotide sequence of the first two genes of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli.";
RL Microb. Pathog. 6:297-309(1989).
RN [3]
RP SEQUENCE OF 24-170 FROM N.A.
RX STRAIN=O78:H11 / H10407;
RA MEDLINE=82235736; PubMed=6124420;
RA Klemm P.;
RT "Primary structure of the CFA/I fimbrial protein from human enterotoxigenic Escherichia coli strains.";
RL Eur. J. Biochem. 124:339-348(1982).
RN [4]
RP SEQUENCE OF 24-42.
RX STRAIN=O78:H11 / H10407;
RA MEDLINE=90036735; PubMed=2572583;
RA Hall R.H., Maneval D.R. Jr., Collins J.H., Theibert J.L.,
RA Levine M.M.;
RT "Purification and analysis of colonization factor antigen I, coli surface antigen 1, and coli surface antigen 3 fimbriae from enterotoxigenic Escherichia coli.";
RL J. Bacteriol. 171:6372-6374(1989).
CC -!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5 MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -!- SUBUNIT: CFA/I FIMBRIAE ARE RATHER RIGID, THREAD-LIKE FILAMENTS OF
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CC 0.5-1 MICROMETER, WITH AN APPARENT AXIAL HOLE, AND A DIAMETER OF
CC 7 NANOMETERS. A SINGLE CFA/I FIMBRIA CONSISTS OF ABOUT 100
CC IDENTICAL PROTEIN SUBUNITS.
CC -!- INDUCTION: CFA/I FIMBRIAE ARE ONLY EXPRESSED IN THE PRESENCE OF
CC THE POSITIVE REGULATOR CFAD.
CC -!- SIMILARITY: TO THE CS1 FIMBRIAL SUBUNIT A (CSOA).
CC
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CC
CC EMBL; M55661; AAC41415.1; -
CC PIR; A30589; YQECCL.
KW Fimbrin; Antigen; Plasmid; Signal.
FT SIGNAL 1 23
FT CHAIN 24 170 CFA/I FIMBRIAL SUBUNIT B.
FT CONFLICT 37 37 V -> A (IN REF. 2).
FT CONFLICT 76 76 D -> N (IN REF. 3).
FT CONFLICT 97 97 S -> A (IN REF. 3).
SQ SEQUENCE 170 AA; 17461 MW; 924347F07F33CDAB CRC64;

Query Match 80.0%; Score 40; DB 1; Length 170;
Best Local Similarity 80.0%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSVALTYSP 10
Db 49 PSVALTYSP 58

RESULT 3
POLN RHDV3
ID POLN_RHDV3 STANDARD; PRT; 234 AA.
AC P27411;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Non-structural polyprotein [Contains: Coat protein] (Fragment).
OS Rabbit hemorrhagic disease virus (strain V-351) (RHDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Lagovirus.
OX NCBI_TaxID=11977;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307403; PubMed=1497750;
RA Milton I.D., Vlasak R., Nowotny N., Rodak L., Carter M.J.;
RT "Genomic 3' terminal sequence comparison of three isolates of rabbit haemorrhagic disease virus.";
RL FEMS Microbiol. Lett. 72:37-42(1992).
CC
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CC
CC EMBL; Z11535; CAA77633.1; -
CC PIR; S22134; S22134.
DR InterPro; IPR004005; Calici.coat.
DR Pfam; PF00915; Calici.coat; 1.
KW Polyprotein; Coat protein.
FT DOMAIN 1 1
FT NON_TER ? 234 COAT PROTEIN.
SQ SEQUENCE 234 AA; 23777 MW; B66018654E2EE05A CRC64;

Query Match 72.0%; Score 36; DB 1; Length 234;
Best Local Similarity 60.0%; Pred. No. 5.2;
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Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVALTYSP 10  
|:|:|:|:|  
Db 84 PNASALTYTP 93

RESULT 4  
ID MTC2\_CHVP1 STANDARD; PRT; 326 AA.  
AC P1118; 084569;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Modification methylease CVAII (EC 2.1.1.72) (Adenine-specific  
DN methyltransferase CVAII) (M.CVAII).  
OS CVAII OR A251R.  
OS Parametrium burearia chlorella virus 1 (PBCV-1).  
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.  
NCBI\_TaxID=10506;  
[1] SEQUENCE FROM N.A.  
RX MEDLINE=93065201; PubMed=1437552;  
RA Zhang Y., Nelson M., Niefeldt J.W., Burbank D.E., van Etten J.L.;  
"Characterization of Chlorella virus PBCV-1 CVAII restriction and  
modification system.";  
Nucleic Acids Res. 20:5351-5356(1992).  
[2] REVISIONS AND SEQUENCE FROM N.A.  
RX MEDLINE=9513167; PubMed=7831789;  
RA Lu Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., van Etten J.L.;  
"Analysis of 45 kb of DNA located at the left end of the chlorella  
RT virus PBCV-1 genome.";  
Virology 206:339-352(1995).  
CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE  
CATG, CAUSES SPECIFIC METHYLATION ON A-2 ON BOTH STRANDS AND  
PROTECTS THE DNA FROM CLEAVAGE BY THE CVAII ENDONUCLEASE.  
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-  
adenosyl-L-homocysteine + DNA 6-methylaminopurine.  
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CC  
CC EMBL; M86639; AAB92381.1; -;  
DR EMBL; U42580; AAC96619.1; -;  
DR PIR; S27901; S27901.  
DR PIR; S35442; S35442.  
REBASE; 3542; M.CVAII.  
InterPro: IPR002294; D12N6\_mtfrase.  
InterPro: IPR002052; N6\_Mtase.  
Pfam: PFO0866; Methyltransf12; 1.  
DR PRINTS; PRO0505; D12N6MTFRASE.  
DR PROSITE; PS00092; N6\_MTASE; 1.  
KM Transferrase; Methyltransferase; Restriction system.  
SQ SEQUENCE 326 AA; 37492 MW; 8CC1FC75D85F0D89 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 326;  
Best Local Similarity 70.0%; Pred. No. 7.5;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSAAVALTYSP 10  
|:|:|:|:|  
Db 95 PGFVLTYP 104

RESULT 5  
VMAI\_P12HT STANDARD; PRT; 377 AA.  
ID VMAI\_P12HT

AC P24266;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE Matrix protein (Membrane protein).  
GN M.  
OS Human parainfluenza 2 virus (strain Toshiba) (PIV-2).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.  
NCBI\_TaxID=11214;  
[1] SEQUENCE FROM N.A.  
RX MEDLINE=91049454; PubMed=2173264;  
RA Kawano M., Bando H., Ohgimoto S., Okamoto K., Kondo K., Tsurudome M.,  
RA Nishio M., Ito Y.;  
RT "Complete nucleotide sequence of the matrix gene of human  
parainfluenza type 2 virus and expression of the M protein in  
bacteria.";  
Virology 179:857-861(1990).  
CC -1- FUNCTION: THE M PROTEIN HAS A CRUCIAL ROLE IN VIRUS ASSEMBLY  
AND INTERACTS WITH THE RNP COMPLEX AS WELL AS WITH THE VIRAL  
MEMBRANE.  
CC  
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CC  
CC EMBL; M62734; AAA46862.1; -;  
DR EMBL; X57559; CAA40785.1; -;  
DR PIR; A36421; MENZP2.  
DR PIR; S16661; S16661.  
InterPro: IPR000982; Matrix.  
DR Pfam; PFO0661; Matrix; 1.  
DR ProDom; PD000741; Matrix; 1.  
KM Matrix protein: Envelope protein.  
SQ SEQUENCE 377 AA; 42312 MW; A181A79C55276736 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 377;  
Best Local Similarity 60.0%; Pred. No. 8.9;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVALTYSP 10  
|:|:|:|:|  
Db 170 PTFVSITYSP 179

RESULT 6  
ID POLN\_RHDV STANDARD; PRT; 2344 AA.  
AC P27410;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Non-structural polypeptide (contains: RNA-directed RNA polymerase  
DE (EC 2.7.7.48); Thiol protease P3C (EC 3.4.22.-); Helicase (2C like  
DE protein); Coat protein).  
OS Rabbit hemorrhagic disease virus (RHDV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
OC Lagovirus.  
NCBI\_TaxID=11976;  
[1] SEQUENCE FROM N.A.  
RX MEDLINE=91361557; PubMed=1440711;  
RA Meyers G., Wirblich C., Thiel H.-J.;  
RT "Rabbit hemorrhagic disease virus - molecular cloning and nucleotide  
sequencing of a calicivirus genome.";  
Virology 184:664-676(1991).  
CC -1- FUNCTION: THE P3C CYSTEINE PROTEASE IS THE PROTEASE RESPONSIBLE  
FOR CLEAVAGE AT CERTAIN Q/G SITES IN THE POLYPROTEIN.  
CC

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CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C24.
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CC -----
DR EMBL; M67473; AAA47285.1; -.
DR PIR; A41039; RRMWRH.
DR MEROPS; C24.001; -.
DR InterPro; IPR004005; Calici_coat.
DR InterPro; IPR004004; Calici_pol_hel.
DR InterPro; IPR000317; Endoptase_C24.
DR InterPro; IPR000605; RNA_helicase.
DR InterPro; IPR001205; RNA_pol_P3D.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00910; RNA_helicase; 1.
DR Pfam; PF00915; Calici_coat; 1.
DR Pfam; PF03510; Peptidase_C24; 1.
DR PRINTS; PR00916; 2CENDOPTASE.
DR PRINTS; PR00918; CALICIVIRUSNS.
DR PolyProtein; Transferase; RNA-directed RNA polymerase; Hydrolase;
KW Thiol protease; Helicase; ATP-binding; Coat protein.
FT CHAIN 2508 2707 HELICASE (P2C-LIKE).
FT CHAIN 1109 1251 PROTEASE P3C.
FT CHAIN ?1497 ?1625 RNA-DIRECTED RNA POLYMERASE.
FT CHAIN ? 2344 COAT PROTEIN.
FT NP_BIND 522 529 ATP (POTENTIAL).
FT ACT_SITE 1212 1212 PROTEASE (POTENTIAL).
FT ACT_SITE 1227 1227 PROTEASE (POTENTIAL).
SQ SEQUENCE 2344 AA; 257066 MW; 1454C248F81E9212 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 2344;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAVALTYSP 10
|:|:|:|:|
Db 2194 PNASAITVTP 2203

RESULT 7
ADH7_HUMAN
ID ADH7_HUMAN STANDARD; PRT; 374 AA.
AC P40394; Q13713;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alcohol dehydrogenase class IV mu/sigma chain (EC 1.1.1.1) (Retinol
DE dehydrogenase) (Gastric alcohol dehydrogenase).
GN ADH7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=94253145; PubMed=8195208;
RA Satre M.A., Zgombic-Knight M., Duester G.;
RT "The complete structure of human class IV alcohol dehydrogenase
RT (retinol dehydrogenase) determined from the ADH7 gene.";
RL J. Biol. Chem. 269:15606-15612(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95181413; PubMed=7876191;
RA Zgombic-Knight M., Foglio M.H., Duester G.;
RT "Genomic structure and expression of the ADH7 gene encoding human

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RT class IV alcohol dehydrogenase, the form most efficient for retinol
RT metabolism in vitro.";
RL J. Biol. Chem. 270:4305-4311(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=95010033; PubMed=7925371;
RA Farres J., Moreno A., Crossas B., Peralba J.M., Allali-Hassani A.,
RA Hjeltnqvist L., Joernvall H., Pares X.;
RT "Alcohol dehydrogenase of class IV (sigma sigma-ADH) from human
RT stomach. cDNA sequence and structure/function relationships.";
RL Eur. J. Biochem. 224:549-557(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=94364515; PubMed=8082805;
RA Yokoyama S., Matsuo Y., Ramsbotham R., Yokoyama R.;
RT "Molecular characterization of a class IV human alcohol dehydrogenase
RT gene (ADH7).";
RL FEBS Lett. 351:411-415(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=95181314; PubMed=7876099;
RA Kedishvili N.Y., Boston W.F., Stone C.L., Hurley T.D., Peggs C.F.,
RA Thomasson H.R., Popov K.M., Carr L.G., Edenberg H.J., Li T.K.;
RT "Expression and kinetic characterization of recombinant human stomach
RT alcohol dehydrogenase. Active-site amino acid sequence explains
RT substrate specificity compared with liver isozymes.";
RL J. Biol. Chem. 270:3625-3630(1995).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Fore skin;
RA Yokoyama H., Baraona E., Lieber C.S.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 227-299 FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=95289593; PubMed=7771649;
RA Cheung B., Anderson J.K., Holmes R.S., Beacham I.R.;
RT "Human stomach class IV alcohol dehydrogenase: molecular genetic
RT analysis.";
RL Alcohol. Clin. Exp. Res. 19:185-186(1995).
RN [8]
RP SEQUENCE OF 12-21; 41-46; 62-80; 85-111; 135-142 AND 169-174.
RX MEDLINE=92275085; PubMed=1592118;
RA Pares X., Cederlund E., Moreno A., Saubi N., Hoeoeg J.-O.,
RA Joernvall H.;
RT "Class IV alcohol dehydrogenase (the gastric enzyme). Structural
RT analysis of human sigma sigma-ADH reveals class IV to be variable and
RT confirms the presence of a fifth mammalian alcohol dehydrogenase
RT class.";
RL FEBS Lett. 303:69-72(1992).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=97373546; PubMed=9228021;
RA Xie P., Parsons S.H., Speckhard D.C., Bosron W.F., Hurley T.D.;
RT "X-ray structure of human class IV sigma sigma alcohol dehydrogenase.
RT Structural basis for substrate specificity.";
RL J. Biol. Chem. 272:18558-18563(1997)
CC -1- FUNCTION: COULD FUNCTION IN RETINOL OXIDATION FOR THE SYNTHESIS OF
CC RETINOIC ACID, A HORMONE IMPORTANT FOR CELLULAR DIFFERENTIATION.
CC MEDIUM-CHAIN (OCTANOL) & AROMATIC (M-NITROBENZALDEHYDE) COMPOUNDS
CC ARE THE BEST SUBSTRATES. ETHANOL IS NOT A GOOD SUBSTRATE BUT AT
CC THE HIGH ETHANOL CONCENTRATIONS REACHED IN THE DIGESTIVE TRACT, IT
CC PLAYS A ROLE IN THE ETHANOL OXIDATION AND CONTRIBUTES TO THE FIRST
CC PASS ETHANOL METABOLISM.
CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
CC NADH.
CC -1- COFACTOR: ZINC.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN STOMACH.

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CC -1- MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S ISOZYMES IN HUMAN:
CC THREE BELONGS TO CLASS-I: ALPHA, BETA, AND GAMMA, ONE TO CLASS-II:
CC PI, ONE TO CLASS-III: CHI, ONE TO CLASS-IV: ADH7 AND ONE TO
CC CLASS-V: ADH6.
CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY. CLASS-IV SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U16293; AAC51351.1; -
DR EMBL: U16286; AAC51351.1; JOINED.
DR EMBL: U16287; AAC51351.1; JOINED.
DR EMBL: U16288; AAC51351.1; JOINED.
DR EMBL: U16289; AAC51351.1; JOINED.
DR EMBL: U16290; AAC51351.1; JOINED.
DR EMBL: U16291; AAC51351.1; JOINED.
DR EMBL: U16292; AAC51351.1; JOINED.
DR EMBL: X76342; CAAS3960.1; -
DR EMBL: X76342; CAAS3960.1; ALT_INIT.
DR EMBL: U07821; AAA19002.1; -
DR EMBL: U09623; AAA82165.1; -
DR EMBL: L47166; AAB38424.1; -
DR EMBL: S77168; AAB34478.1; -
DR PIR: S21170; S21170.
DR PDB: 1AGN; 12-MAR-97.
DR Genew: HGNC:256; ADH7.
DR MIM: 600086; -
DR InterPro: IPR002328; ADH_zinc.
DR InterPro: IPR002085; Adh_zn_family.
DR Pfam: PF00107; adh_zinc; 1.
DR PROSITE: PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Zinc; NAD; Multigene family; 3D-structure.
FT METAL 47 47 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 68 68 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 98 98 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 101 101 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 104 104 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 112 112 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 174 174 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 20 20 Q -> R (IN REF. 5).
FT CONFLICT 71 71 T -> R (IN REF. 5).
FT CONFLICT 98 98 C -> V (IN REF. 6).
FT CONFLICT 138 139 HH -> GR (IN REF. 7).
FT CONFLICT 148 149 EY -> VI (IN REF. 6).
FT CONFLICT 157 157 V -> E (IN REF. 6).
FT CONFLICT 205 205 L -> V (IN REF. 6).
SEQUENCE 374 AA; 40005 MW; 1D785CD022C8D387 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 374;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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GN ADH7 OR ADH3 OR ADH-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid:10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Gastric mucosa;
RX MEDLINE=95256259; Pubmed=7738026;
RA Zgonibic-Knight M., Ang H.L., Foglio M.H., Duester G.;
RA Duester G.;
RT "Gene structure and promoter for Adh-3 encoding mouse class IV alcohol
RT dehydrogenase (retinol dehydrogenase).";
RT murine Adh gene family.";
RL J. Biol. Chem. 270:10868-10877 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=129/SvJ.
RX MEDLINE=97271563; Pubmed=9126489;
RA Zgonibic-Knight M., Deltour L., Haselbeck R.J., Foglio M.H.,
RA Duester G.;
RT "Gene structure and promoter for Adh-3 encoding mouse class IV alcohol
RT dehydrogenase (retinol dehydrogenase).";
RL Genomics 41:105-109 (1997).
CC -1- FUNCTION: COULD FUNCTION IN RETINOL OXIDATION FOR THE SYNTHESIS OF
CC RETINOIC ACID, A HORMONE IMPORTANT FOR CELLULAR DIFFERENTIATION.
CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
CC NADH.
CC -1- COFACTOR: ZINC.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE STOMACH MUCOSA. LOWER
CC EXPRESSION IN EYE, THYMUS, SKIN AND OVARY. VERY LOW EXPRESSION IN
CC SMALL INTESTINE, LIVER AND UTERUS.
CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY. CLASS-IV SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: U20257; AAA76735.1; -
DR EMBL: U76734; AAC53124.1; -
DR EMBL: U76728; AAC53124.1; JOINED.
DR EMBL: U76729; AAC53124.1; JOINED.
DR EMBL: U76730; AAC53124.1; JOINED.
DR EMBL: U76727; AAC53124.1; JOINED.
DR EMBL: U76731; AAC53124.1; JOINED.
DR EMBL: U76733; AAC53124.1; JOINED.
DR EMBL: U76732; AAC53124.1; JOINED.
DR HSSP: P40394; 1AGN.
DR MGD: MGI:87926; Adh3.
DR InterPro: IPR002328; ADH_zinc.
DR InterPro: IPR002085; Adh_zn_family.
DR Pfam: PF00107; adh_zinc; 1.
DR PROSITE: PS00059; ADH_ZINC; 1.
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SEQUENCE 374 AA; 39837 MW; 6E0978B44E02D027 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 374;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 PSVAULTYSP 10
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Db 296 PSKMLTYDP 305

RESULT 9
RTG3 YEAST
ID RTG3 YEAST STANDARD; PRT; 486 AA.
AC P38165; P89494;
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15 JUN-2002 (Rel. 41, Last annotation update)
DE Retrograde regulation protein 3.
GN RTG3 OR YBL108C OR YBL0810.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
[1]
RN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
RP STRAIN=Oregon-R; TISSUE=Embryo, Larva, and Pupae;
RX MEDLINE=20337577; PubMed=10772791;
RA Pecasse F., Beck Y., Ruiz C., Richards G.;
RT "Kruppel-homolog, a stage-specific modulator of the prepupal ecdysone
response, is essential for Drosophila metamorphosis.";
RL Dev. Biol. 221:53-67(2000).
[2]
RN SEQUENCE FROM N.A. (ALPHA AND BETA ISOPROFORMS).
RP STRAIN=Berkely; PubMed=10731132;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anandates P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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QY 1 PSVAULTYSP 10
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Db 296 PSKMLTYDP 305

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DE Retrograde regulation protein 3.
GN RTG3 OR YBL108C OR YBL0810.
OS Saccharomyces cerevisiae (Baker's yeast).
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QY 1 PSVAULTYSP 10
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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 RN SEQUENCE OF 289-367 FROM N.A.  
 RP MEDLINE=87051757; PubMed=3096579;  
 RA Schuh R., Aicher W., Gaul U., Cote S., Preiss A., Maier D.,  
 RA Seifert E., Naber W., Schroeder C., Kemler R., Jaekel H.,  
 RT "A conserved family of nuclear proteins containing structural  
 RT elements of the finger protein encoded by Kruppel, a Drosophila  
 RT segmentation gene.";  
 RL Cell 47:1025-1032(1986).  
 CC -1- FUNCTION: PLAYS A GENERAL ROLE IN THE HIERARCHIES OF GENE  
 CC EXPRESSION LEADING TO METAMORPHOSIS.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOMORPHS; ALPHA AND BETA (SHOWN HERE); ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- DEVELOPMENTAL STAGE: BETA ISOFORM IS EXPRESSED DURING  
 CC EMBRYOGENESIS, MOST ABUNDANT IN MIDEMBRYOGENESIS, AND IN ADULTS.  
 CC ALPHA ISOFORM IS EXPRESSED FROM EMBRYOGENESIS TO 8 HOURS AFTER  
 CC PUPARIATION, MAJOR PERIOD OF EXPRESSION IS DURING SECOND INSTAR.  
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL: AJ005440; CA006543.2; -  
 DR EMBL: AJ005441; CA006544.2; -  
 DR EMBL: AE003612; AAF52343.2; -  
 DR EMBL: AE003612; AAG22417.1; -  
 DR EMBL: M14940; AAA28660.1; -  
 DR HSSP: P08047; ISP2.  
 DR FlyBase: FBgn0028420; Kr-h1.  
 DR InterPro: IPR000822; Znf\_C2H2.  
 DR Pfam: PF00096; Zf\_C2H2; 8.  
 DR ProDom: PD000003; Znf\_C2H2; 4.  
 DR SMART: SM00355; Znf\_C2H2; 8.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 8.  
 DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 8.  
 DR Zinc-Finger; Metal-binding; DNA-binding; Repeat; Alternative splicing;  
 KW Developmental protein.  
 FT DOMAIN 108 148 GLN-RICH.  
 FT DOMAIN 482 515 SER/THR-RICH.  
 FT DOMAIN 538 565 SER/THR-RICH.  
 FT DOMAIN 194 463 ZINC-FINGERS.  
 FT ZN\_FING 194 463 C2H2-TYPE.  
 FT ZN\_FING 271 293 C2H2-TYPE.  
 FT ZN\_FING 299 321 C2H2-TYPE.  
 FT ZN\_FING 327 349 C2H2-TYPE.  
 FT ZN\_FING 355 377 C2H2-TYPE.  
 FT ZN\_FING 383 407 C2H2-TYPE.  
 FT ZN\_FING 413 435 C2H2-TYPE.  
 FT ZN\_FING 441 463 C2H2-TYPE.  
 FT VARSPIC 1 54 MISSING (IN ISOFORM ALPHA).  
 FT CONFLICT 313 313 N->D (IN REF. 3).  
 SO SEQUENCE 845 AA; 91451 MW; A4D87839DCEB372 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 845;  
 Best Local Similarity 60.0%; Pred. No. 34;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVLTISP 10  
 DB 544 PSSUSTYSP 553

RESULT 11  
 CHS2\_YEAST STANDARD; PRT; 963 AA.  
 AC P14180;  
 DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Chitin synthase 2 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosamine)  
 DE transferase 2).  
 GN CHS2 OR YBR038W OR YBR0407.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90143137; PubMed=2533436;  
 RA Silverman S.J.;  
 RT "Similar and different domains of chitin synthases 1 and 2 of S.  
 RT cerevisiae: two isoforms with distinct functions.";  
 RL Yeast 5:459-467(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=S288c;  
 RA Andrie B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,  
 RA Vissers S.;  
 RN Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP MUTAGENESIS.  
 RP MEDLINE=95293998; PubMed=7775457;  
 RA Nagahashi S., Sudoh M., Ono N., Sawada R., Yamaguchi E., Uchida Y.,  
 RA Mio T., Takagi M., Arita M., Yamada-Okabe H.;  
 RT "Characterization of chitin synthase 2 of Saccharomyces cerevisiae.  
 RT Implication of two highly conserved domains as possible catalytic  
 RT sites.";  
 RL J. Biol. Chem. 270:13961-13967(1995).  
 CC -1- FUNCTION: ESSENTIAL FOR SEPTUM FORMATION AND CELL DIVISION. CHS2  
 CC IS REQUIRED FOR MAINTAINING NORMAL CELL MORPHOLOGY.  
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + {(1,4) (N-acetyl)-  
 CC beta-D-glucosamine}[(N) = UDP + {(1,4) (N-acetyl)-beta-D-  
 CC glucosamine}[(N+1)].  
 CC -1- ENZYME REGULATION: REQUIRES PROTEOLYTIC ACTIVATION.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M23865; AAA34493.1; -  
 DR EMBL: Z35907; CAAB4980.1; -  
 DR PIR: S45167; S45167.  
 DR PIR: A30922; A30922.  
 DR SGD: S0000242; CHS2.  
 DR InterPro: IPR004834; Chitin synth.  
 DR InterPro: IPR001173; Glycosyltransf.  
 DR Pfam: PF01644; Chitin synth. 1.  
 DR ProDom: PD002998; Chitin synth. 1.  
 DR Transferase; Glycosyltransferase; Transmembrane; Cell wall;  
 KW Multigene family.  
 FT DOMAIN 1 422 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 423 443 1 (POTENTIAL).  
 FT DOMAIN 444 643 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 644 664 2 (POTENTIAL).  
 FT DOMAIN 665 677 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 678 698 3 (POTENTIAL).  
 FT DOMAIN 699 711 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 712 732 4 (POTENTIAL).  
 FT DOMAIN 733 743 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 744 764 5 (POTENTIAL).  
 FT DOMAIN 765 775 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 776 796 6 (POTENTIAL).  
 FT DOMAIN 797 875 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 876 896 7 (POTENTIAL).

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FT DOMAIN 897 905
FT TRANSMEM 906 926
FT DOMAIN 927 963
FT MUTAGEN 197 197
FT MUTAGEN 312 312
FT MUTAGEN 355 355
FT MUTAGEN 393 393
FT MUTAGEN 441 441
FT MUTAGEN 441 441
FT MUTAGEN 447 447
FT MUTAGEN 490 490
FT MUTAGEN 492 492
FT MUTAGEN 493 493
FT MUTAGEN 494 494
FT MUTAGEN 497 497
FT MUTAGEN 502 502
FT MUTAGEN 505 505
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FT MUTAGEN 563 563
FT MUTAGEN 563 563
FT MUTAGEN 565 565
FT MUTAGEN 589 589
FT MUTAGEN 592 592
FT MUTAGEN 601 601
FT MUTAGEN 601 601
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FT MUTAGEN 607 607
SQ SEQUENCE 963 AA; 109881 MW; 4D4A287C0B65B5B CRC64;

Query Match 70.0%; Score 35; DB 1; Length 963;
Best Local Similarity 70.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10
Db 61 PSRAALRYSP 70

RESULT 12
LRAA HUMAN
AC P50851; Q9H204; Q9H203;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15 JUN 2002 (Rel. 41, Last sequence update)
DT 15 JUN 2002 (Rel. 41, Last annotation update)
DE Lipopolysaccharide-responsive and beige-like anchor protein (CDC4-like
DE protein) (Beige-like protein).
GN LRAA OR LRA OR CDC4L OR BGL.

CYTOPLASMIC (POTENTIAL).
8 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
N->A: 30% DECREASE OF ACTIVITY.
S->A: 20% INCREASE OF ACTIVITY.
D->A: 10% INCREASE OF ACTIVITY.
D->A: 5% DECREASE OF ACTIVITY.
D->A: LOSS OF ACTIVITY.
D->E: LOSS OF ACTIVITY.
Q->A: 80% DECREASE OF ACTIVITY.
N->A: 80% DECREASE OF ACTIVITY.
P->A: 80% DECREASE OF ACTIVITY.
E->A: 90% DECREASE OF ACTIVITY.
Y->A: 95% DECREASE OF ACTIVITY.
S->A: 95% DECREASE OF ACTIVITY.
K->A: 90% DECREASE OF ACTIVITY.
E->A: 80% INCREASE OF ACTIVITY.
S->A: 20% INCREASE OF ACTIVITY.
F->A: 60% DECREASE OF ACTIVITY.
G->A: 70% DECREASE OF ACTIVITY.
L->A: 80% DECREASE OF ACTIVITY.
P->A: 90% DECREASE OF ACTIVITY.
G->A: 95% DECREASE OF ACTIVITY.
Y->A: LOSS OF ACTIVITY.
R->A: 60% DECREASE OF ACTIVITY.
R->A: NO CHANGE IN ACTIVITY.
H->A: 85% DECREASE OF ACTIVITY.
N->A: 95% DECREASE OF ACTIVITY.
L->A: 95% DECREASE OF ACTIVITY.
E->A: LOSS OF ACTIVITY.
E->A: 65% DECREASE OF ACTIVITY.
E->Q: LOSS OF ACTIVITY.
D->A: LOSS OF ACTIVITY.
D->E: LOSS OF ACTIVITY.
D->N: LOSS OF ACTIVITY.
R->A: LOSS OF ACTIVITY.
R->K: 94% DECREASE OF ACTIVITY.
L->A: 95% DECREASE OF ACTIVITY.
T->A: 70% DECREASE OF ACTIVITY.
P->A: 70% DECREASE OF ACTIVITY.
Q->A: LOSS OF ACTIVITY.
Q->N: LOSS OF ACTIVITY.
R->A: LOSS OF ACTIVITY.
R->K: 95% DECREASE OF ACTIVITY.
R->A: LOSS OF ACTIVITY.
R->K: 57% DECREASE OF ACTIVITY.
RR->KK: LOSS OF ACTIVITY.
R->A: LOSS OF ACTIVITY.
W->A: LOSS OF ACTIVITY.
W->Y: LOSS OF ACTIVITY.
N->A: 95% DECREASE OF ACTIVITY.

Query Match 70.0%; Score 35; DB 1; Length 963;
Best Local Similarity 70.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10
Db 61 PSRAALRYSP 70

RESULT 12
LRAA HUMAN
AC P50851; Q9H204; Q9H203;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15 JUN 2002 (Rel. 41, Last sequence update)
DT 15 JUN 2002 (Rel. 41, Last annotation update)
DE Lipopolysaccharide-responsive and beige-like anchor protein (CDC4-like
DE protein) (Beige-like protein).
GN LRAA OR LRA OR CDC4L OR BGL.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21154060; PubMed=11254716;
RA Wang J.-W., Howson J., Haller E., Kerr W.G.;
RT "Identification of a novel lipopolysaccharide-inducible gene with key
RL features of both A kinase anchor proteins and chsl/beige proteins.";
RN J. Immunol. 166:4586-4595(2001).
RP [2]
RP SEQUENCE OF 775-2692 FROM N.A.
RA Mager D.L.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 2179-2692 FROM N.A.
RX MEDLINE=92372019; PubMed=1505956;
RA Feuchter A.E., Freeman J.D., Mager D.L.;
RT "Strategy for detecting cellular transcripts promoted by human
RL endogenous long terminal repeats: Identification of a novel gene
RL (CDC4L) with homology to Yeast CDC4.";
RN Genomics 13:1237-1246(1992).
CC -!- INDUCTION: By lipopolysaccharide (LPS).
CC -!- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: CONTAINS 1 BEACH DOMAIN.
CC -!- CAUTION: WAS ORIGINALLY (REF.3) SAID TO BE SIMILAR TO YEAST (CDC4,
CC BUT THAT SIMILARITY IS VERY LIMITED.
CC -----
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CC -----
DR EMBL; AF216648; AAG48558.2; -
DR EMBL; AF217149; AAG48559.1; -
DR EMBL; M83822; AAB09603.1; -
DR Genew; HGNC:1742; LRBA.
DR MIM; 606453; -
DR InterPro; IPR000409; Beige_BEACH.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 10.
DR Pfam; PF02138; Beach; 3.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS50197; BEACH; 1.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE NEG.
DR PROSITE; PS50082; WD_REPEATS_2; FALSE NEG.
DR PROSITE; PS50294; WD_REPEATS_REGION; FALSE NEG.
KW Repeat; WD repeat.
FT REPEAT 1301 1343 WD 1.
FT DOMAIN 2219 2489 BEACH.
FT REPEAT 2591 2633 WD 2.
FT REPEAT 2636 2679 WD 3.
FT REPEAT 2695 2735 WD 4.
FT REPEAT 2777 2816 WD 5.
FT REPEAT 2819 2858 WD 6.
FT CONFLICT 2674 2692
SQ SEQUENCE 2863 AA; 319157 MW; D58EE93A6E924C30 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 2863;
Best Local Similarity 66.7%; Pred. No. 13e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SAVALTYSP 10
Db 415 SAIAFTYNP 423

RESULT 13

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ANPC\_HUMAN STANDARD; PRT; 540 AA.  
 ID ANPC\_HUMAN  
 AC P17342;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Atrial natriuretic peptide clearance receptor precursor (ANP-C)  
 DE (ANP-C) (Atrial natriuretic peptide C-type receptor).  
 OS Homo sapiens (Human).  
 GN NRP3 OR ANP-C.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=90287735; PubMed=2162522;  
 RA Lowe D.G., Camerato T.R., Goeddel D.V.;  
 RT "cDNA sequence of the human atrial natriuretic peptide clearance  
 receptor.";  
 RL Nucleic Acids Res. 18:3412-3412(1990).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90386656; PubMed=2169733;  
 RA Porter D.G., Attesten A., Fuller F., Miller J.A., Gregory L.C.,  
 Lewicki J.A.;  
 RT "Isolation and functional expression of the human atrial natriuretic  
 peptide clearance receptor cDNA.";  
 RL Biochem. Biophys. Res. Commun. 171:796-803(1990).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lens epithelium;  
 RA Rae J.L., Shepard A.R.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases  
 CC -1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. DOES NOT HAVE  
 GUANYLATE CYCLASE ACTIVITY.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO  
 WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C)  
 WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE  
 CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.  
 CC -1- SIMILARITY: TO ANP-A AND ANP-B RECEPTORS IN THEIR EXTRACELLULAR  
 AND TRANSMEMBRANE DOMAINS.  
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 EMBL: X52282; CAA36523.1;  
 EMBL: M59305; AAA51734.1;  
 EMBL: AF025998; AAB88801.1;  
 DR PIR: S10150; S10150.  
 DR PIR: S15896; A35896.  
 DR Genew: HGNC:7945; NRP3.  
 DR MIM: 108962;  
 DR InterPro: IPR001828; ANP\_receptor.  
 DR InterPro: IPR001170; Ntpep\_receptor.  
 DR Pfam: PF01094; ANP\_receptor; 1.  
 DR PRINTS: PR00255; NATPEPTIDER.  
 DR PROSITE: PS00458; ANP\_RECEPTORS; 1.  
 DR Receptor: Glycoprotein; Transmembrane; Signal.  
 FT CHAIN 1 18 ATRIAL NATRIURETIC PEPTIDE CLEARANCE  
 FT SIGNAL 1 18 RECEPTOR.  
 FT DOMAIN 19 480 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 481 503 POTENTIAL.  
 FT DOMAIN 504 540 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 108 136 BY SIMILARITY.

FT DISULFID 213 261 BY SIMILARITY.  
 FT DISULFID 473 473 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 476 476 C -> SG (IN REF. 2).  
 SQ SEQUENCE 540 AA; 59766 MW; 53EE020A296D6F5 CRC64;  
 Query Match 68.0%; Score 34; DB 1; Length 540;  
 Best Local Similarity 60.0%; Pred. No. 33;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 PSAVALTSP 10  
 Db 2 PSLVLTSP 11  
 RESULT 14  
 ID DVL2\_MOUSE STANDARD; PRT; 736 AA.  
 AC Q60838;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Segment polarity protein dishevelled homolog DVL-2 (Dishevelled-2)  
 DE (DSH homolog 2).  
 GN DVL2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BA1B/C; TISSUE=Brain;  
 RX MEDLINE=97042042; PubMed=8897313;  
 RA KligenSmith J., Yang Y., Axelrod J.D., Beier D.R., Ferrimon N.,  
 Sussman D.J.;  
 RT "Conservation of dishevelled structure and function between flies and  
 mice: isolation and characterization of Dvl2.";  
 RL Mech. Dev. 58:15-26(1996).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY  
 MEDIATED BY MULTIPLE WNT GENES.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.  
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
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 EMBL: U24160; AAC52827.1;  
 DR HSPF: Q12923; 3PDZ.  
 DR WGD: MG1:106613; DVL2.  
 DR InterPro: IPR000591; DEP.  
 DR InterPro: IPR001158; DIX.  
 DR InterPro: IPR003351; Dishevelled.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ; 1.  
 DR Pfam: PF00610; DEP; 1.  
 DR Pfam: PF00778; DIX; 1.  
 DR Pfam: PF02377; Dishevelled; 1.  
 DR Prodom: PD003639; DIX; 1.  
 DR SMART: SM00021; DAX; 1.  
 DR SMART: SM00043; DEP; 1.  
 DR SMART: SM00228; PDZ; 1.  
 DR PROSITE: PS50186; DEP; 1.  
 DR PROSITE: PS50106; PDZ; 1.

KW Developmental protein.  
 FT DOMAIN 7 12 POLY-GLY.  
 FT DOMAIN 112 122 POLY-PRO.  
 FT DOMAIN 235 240 POLY-ARG.  
 FT DOMAIN 267 339 PDZ.  
 FT DOMAIN 433 507 DEP.  
 FT DOMAIN 686 691 POLY-PRO.  
 SQ SEQUENCE 736 AA; 78802 MW; 9237C3D3D3C92A60 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 736;  
 Best Local Similarity 66.7%; Pred. No. 47;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSVAALTYSP 10  
 ||| |  
 Db 670 PS3MALPYNP 679

RESULT 15  
 ID BL14 CAEEL STANDARD; PRT; 943 AA.  
 AC P51559; 044762; 044763; 044764; 044765; 044766;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Endoprotease bli-4 precursor (EC 3.4.21.-) (Blisterase) (Blistered  
 DE cuticle protein 4).  
 GN BLI-4 OR K04F10.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 CX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D), AND FUNCTION.  
 RC STRAIN Bristol N2;  
 RX MEDLINE=96293228; PubMed=7774813;  
 RA Thacker C., Peters K.W., Strayko M., Rose A.M.;  
 RT "The bli 4 locus of Caenorhabditis elegans encodes structurally  
 RT distinct kex2/subtilisin-like endoproteases essential for early  
 RT development and adult morphology";  
 RL Genes Dev. 9:956-971(1995).  
 RN [2]  
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RP STRAIN Bristol N2;  
 RC Latreille P., Wamsley P.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 CC 1 FUNCTION: Isoform A is required for normal production or  
 CC maintenance of the adult cuticle. There is functional redundancy  
 CC between the isoforms. Vital for embryonic and larval development.  
 CC 2 TISSUE SPECIFICITY: In larvae and adults, expressed in all  
 CC hypodermal cells, vulva and ventral nerve cords.  
 CC 3 DEVELOPMENTAL STAGE: Expression starts at embryo two-fold stage  
 CC through to adults.  
 CC 4 ALTERNATIVE PRODUCTS: 5 isoforms; A/a, B/b, C/c, D/d (shown here)  
 CC and e; may be produced by alternative splicing.  
 CC 5 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. PURIN SUBFAMILY.  
 CC 6 CAUTION: Ref.1 sequence differs from that shown due to a  
 CC frameshift in position 651.  
 CC 7 CAUTION: Ref.2 (AAB96754/AAB96757) sequence differs from that  
 CC shown due to erroneous gene model prediction.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; L29438; AAA98750.1; ALT\_FRAME.  
 EMBL; L29439; AAA98751.1; ALT\_FRAME.  
 EMBL; L29440; AAA98752.1; ALT\_FRAME.  
 EMBL; AF039719; AAB96753.1; -.

DR EMBL; AF039719; AAB96754.1; ALT\_SEQ.  
 DR EMBL; AF039719; AAB96755.1; -.  
 DR EMBL; AF039719; AAB96756.1; -.  
 DR EMBL; AF039719; AAB96757.1; ALT\_SEQ.  
 DR MEROPS; S08\_031; -.  
 DR WormPep; K04F10.4a; CE11728.  
 DR WormPep; K04F10.4b; CE11730.  
 DR WormPep; K04F10.4c; CE11732.  
 DR WormPep; K04F10.4d; CE11734.  
 DR WormPep; K04F10.4e; CE11736.  
 DR InterPro; IPR002884; P domain.  
 DR InterPro; IPR002029; Peptidase\_S8.  
 DR Pfam; PF00082; Peptidase\_S8; 1.  
 DR Pfam; PF01483; P; PARTIAL.  
 DR PRINTS; PRO00723; SUBTILISIN.  
 DR ProDom; PD000717; P domain; 1.  
 DR PROSITE; PS00136; SUBTILASE ASP; 1.  
 DR PROSITE; PS00137; SUBTILASE\_HIS; 1.  
 DR PROSITE; PS00138; SUBTILASE\_SER; 1.  
 KW Hydrolyase; Serine protease; Glycoprotein; Calcium-binding; Zymoqen;  
 KW Transmembrane; Signal; Alternative splicing.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT PROPEP 21 116 BY SIMILARITY.  
 FT CHAIN 117 943 ENDOPROTEASE BLI-4.  
 FT ACT\_SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 241 241 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 415 415 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT TRANSMEM 417 437 POTENTIAL.  
 FT DOMAIN 438 684 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 713 857 CYS-RICH.  
 FT CATHODYD 195 195 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPPLIC 658 670 VEESARSPFDLT -> ILITIAHLVNA (IN  
 FT VARSPPLIC 658 699 VEESARSPFDLTSGMKLSGDCNGGCTESSATSCFAYKH  
 FT L -> LCFNFENSQTCVCLVCHVPGVINFQIEKLLKST  
 FT KCLIFS (IN ISOFORM E).  
 FT VEESARSPFDLTSGMKLSGDCNGGCTESSATSCFAYKH  
 FT LTQTLNRKGGSGFKVQKDDTYLLDGKCKM -> GDEVV  
 FT ERIRHWEVTLESSHWNWEHREHKSLOELNSSSRTHSFL  
 FT YSFTKFPQIFLLILVCLFDIHIQFAV (IN ISOFORM  
 FT B).  
 FT VARSPPLIC 671 943 MISSING (IN ISOFORM A).  
 FT VARSPPLIC 700 943 MISSING (IN ISOFORM E).  
 FT VARSPPLIC 731 943 MISSING (IN ISOFORM B).  
 FT VARSPPLIC 780 828 ESNLYQAKCMIRKDLGCGYINAVGKDLCSSTETCTAP  
 FT GPMSCCKC -> AENPDCAKNNSGRODTTFVKFKKRAAF  
 FT KDVCNKLVDLDFPIFLF (IN ISOFORM C).  
 FT VARSPPLIC 829 943 MISSING (IN ISOFORM C).  
 FT CONFLICT 153 153 A -> R (IN REF. 2).  
 FT CONFLICT 346 346 S -> R (IN REF. 2).  
 SQ SEQUENCE 943 AA; 103146 MW; 401E009E6C46AD7E CRC64;

Query Match 68.0%; Score 34; DB 1; Length 943;  
 Best Local Similarity 66.7%; Pred. No. 62;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSVAALTYSP 9  
 ||| |  
 Db 381 PSSIAITYTS 389

RESULT 16  
 CINS\_HUMAN STANDARD; PRT; 2016 AA.  
 ID\_CIN5 HUMAN  
 AC O14524;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Sodium channel protein, cardiac muscle alpha-subunit (HHL1).  
 GN SCN5A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RT MEDLINE=92115699; PubMed=1309946;  
 RA Gellens M.E., George A.L. Jr., Chen L.O., Chahine M., Horn R.,  
 RA Barclay R.L., Kallen R.G.;  
 RT "Primary structure and functional expression of the human cardiac  
 RT tetrodotoxin-insensitive voltage-dependent sodium channel.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:554-558(1992).  
 RN [2]  
 RP VARIANTS LQTS.  
 RX MEDLINE=95196273; PubMed=7889574;  
 RA Wang Q., Shen J., Splawski I., Atkinson D., Li Z., Robinson J.L.,  
 RA Moss A.J., Towbin J.A., Keating M.T.;  
 RT "SCN5A mutations associated with an inherited cardiac arrhythmia, long  
 RT QT syndrome.";  
 RL Cell 80:805-811(1995).  
 RN [3]  
 RP VARIANTS LQTS.  
 RX MEDLINE=96081224; PubMed=8541846;  
 RA Wang Q., Shen J., Li Z., Timothy K., Vincent G.M., Priori S.G.,  
 RA Schwartz P.J., Keating M.T.;  
 RT "Cardiac sodium channel mutations in patients with long QT syndrome,  
 RT an inherited cardiac arrhythmia.";  
 RL Hum. Mol. Genet. 4:1603-1607(1995).  
 RN [4]  
 RP VARIANT LQTS 1505-LYS--GLN-1507 DEL.  
 RX MEDLINE=95179949; PubMed=7651517;  
 RA Bennett P.B., Yazawa K., Makita N., George A.L. Jr.;  
 RT "Molecular mechanism for an inherited cardiac arrhythmia.";  
 RL Nature 376:683-685(1995).  
 RN [5]  
 RP VARIANT LQTS GLY-1790.  
 RX MEDLINE=98349542; PubMed=9686753;  
 RA An R.H., Wang X.L., Kerem B., Benhorin J., Medina A., Goldmit M.,  
 RA Kass R.S.;  
 RT "Novel LQT-3 mutation affects Na<sup>+</sup> channel activity through  
 RT interactions between alpha- and beta-subunits.";  
 RL Circ. Res. 83:141-146(1998).  
 RN [6]  
 RP VARIANT LQTS GLN-1623.  
 RX MEDLINE=98165676; PubMed=9506831;  
 RA Makita N., Shirai N., Nagashima M., Matsuo K., Yamada Y., Tohse N.,  
 RA Kitabatake A.;  
 RT "A de novo missense mutation of human cardiac Na(+) channel exhibiting  
 RT novel molecular mechanisms of long QT syndrome.";  
 RL FEBS Lett. 423:5-9(1998).  
 RN [7]  
 RP VARIANT LQTS GLY-1839.  
 RA Benhorin J., Goldmit M., Maccluer J.M., Blangero J., Goffen R.,  
 RA Leibovich A., Rahat A., Wang Q., Medina A., Towbin J., Kerem B.;  
 RT "Identification of a new SCN5A mutation, D1840G, associated with the  
 RT long QT syndrome.";  
 RL Hum. Mutat. 12:72-72(1998).  
 RN [8]  
 RP VARIANT LQTS GLN-1623.  
 RA Yamauchi H., Furutani M., Kamisago M., Morikawa Y., Kojima Y.,  
 RA Hino Y., Furutani Y., Kimura M., Imamura S.-I., Takao A., Momma K.,  
 RA Matsuo K.;  
 RT "A de novo missense mutation (R1623Q) of the SCN5A gene in a Japanese  
 RT girl with sporadic long QT syndrome.";  
 RL Hum. Mutat. 12:481-481(1998).  
 RN [9]  
 RP VARIANTS LQTS MET-1304 AND MET-1645, AND VARIANT ASN-1500.  
 RX MEDLINE=99439526; PubMed=10508990;  
 RA Watanabe-Ichikawa D., Vesely M.R., Duggal P., Levine J.C.,  
 RA Blume E.D., Wolff G.S., Edwards S.B., Beggs A.H.;  
 RT "Sodium channel abnormalities are infrequent in patients with long QT  
 RT syndrome: identification of two novel SCN5A mutations.";  
 RL Am. J. Med. Genet. 86:470-476(1999).  
 RN [10]  
 RP VARIANT LQTS LYS-1784.

RX MEDLINE=99307063; PubMed=10377081;  
 RA Wei J., Wang D.W., Alings M., Fish F., Wathen M., Roden D.M.,  
 RA George A.L. Jr.;  
 RT "Congenital long-QT syndrome caused by a novel mutation in a conserved  
 RT acidic domain of the cardiac Na<sup>+</sup> channel.";  
 RL Circulation 99:3165-3171(1999).  
 RN [11]  
 RP VARIANTS LQTS N-1114; V-1501; L-1623; H-1644 AND N-1787.  
 RX MEDLINE=20432616; PubMed=10973849;  
 RA Splawski I., Shen J., Timothy K.W., Lehmann M.H., Priori S.,  
 RA Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vincent G.M.,  
 RA Keating M.T.;  
 RT "Spectrum of mutations in long-QT syndrome genes. KVLQT1, HERG, SCN5A,  
 RT KCNE1, and KCNE2.";  
 RL Circulation 102:1178-1185(2000).  
 CC - FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION  
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE  
 CC MEMBRANE. THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH  
 CC WHICH NA<sup>+</sup> IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL  
 CC GRADIENT. IT IS A TETRODOTOXIN-RESISTANT NA<sup>+</sup> CHANNEL ISOFORM. THIS  
 CC CHANNEL IS RESPONSIBLE FOR THE INITIAL UPSTROKE OF THE ACTION  
 CC POTENTIAL IN THE ELECTROCARDIOGRAM.  
 CC - SUBCELLULAR LOCATION: Integral membrane protein.  
 CC - TISSUE SPECIFICITY: EXPRESSED IN HUMAN ATRIAL AND VENTRICULAR  
 CC CARDIAC MUSCLE BUT NOT IN ADULT SKELETAL MUSCLE, BRAIN,  
 CC MYOMETRIUM, LIVER, OR SPLEEN.  
 CC - DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5  
 CC HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED  
 CC SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE  
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT  
 CC EVERY THIRD POSITION.  
 CC - DISEASE: DEFECTS IN SCN5A ARE THE CAUSE OF LONG QT SYNDROME TYPE 3  
 CC (LQTS). AN AUTOSOMAL DOMINANT CARDIAC DISEASE CHARACTERIZED BY  
 CC RECURRENT SYNCOPE AND SUDDEN CARDIAC DEATH.  
 CC - MISCELLANEOUS: NA<sup>+</sup> CHANNELS IN MAMMALIAN CARDIAC MEMBRANE HAVE  
 CC FUNCTIONAL PROPERTIES QUITE DISTINCT FROM NA<sup>+</sup> CHANNELS IN NERVE  
 CC AND SKELETAL MUSCLE.  
 CC - SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.  
 CC - SIMILARITY: CONTAINS 1 IO DOMAIN.  
 CC - DATABASE: NAME=LQTSdb; NOTE=SCN5A mutations page;  
 CC WWW="http://www.ssi.dk/en/forkeking/lqtsdb/scn5a.htm".  
 CC -----  
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 CC -----  
 DR EMBL, M77235; AAA58644.1; -  
 DR Genbank, HGNC:10593; SCN5A.  
 DR MIM: 600163; -  
 DR InterPro: IPR001682; Ca/Na\_pore.  
 DR InterPro: IPR002111; Cat channel\_Tryp.  
 DR InterPro: IPR000048; IQ\_region.  
 DR InterPro: IPR000636; M\_channel\_nlg.  
 DR InterPro: IPR001696; Na\_channel.  
 DR Pfam: PF00520; Ion\_trans; 4.  
 DR Pfam: PF00612; IQ\_1.  
 DR PRINTS: PRO0170; NACHANNEL.  
 DR SMART: SM00015; IQ\_1.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Glycoprotein; Repeat; Multigene family; Phosphorylation;  
 KW Polymorphism; Disease mutation; Long QT syndrome.  
 FT TRANSMEM 127 150  
 FT TRANSMEM 159 178  
 FT TRANSMEM 192 210  
 FT TRANSMEM 217 236  
 FT TRANSMEM 253 276  
 FT TRANSMEM 390 415  
 FT TRANSMEM 712 736  
 ST OF REPEAT I (POTENTIAL).  
 S2 OF REPEAT I (POTENTIAL).  
 S3 OF REPEAT I (POTENTIAL).  
 S4 OF REPEAT I (POTENTIAL).  
 S5 OF REPEAT I (POTENTIAL).  
 S6 OF REPEAT I (POTENTIAL).  
 S1 OF REPEAT II (POTENTIAL).

```

FT TRANSMEM 748 771 S2 OF REPEAT I1 (POTENTIAL).
FT TRANSMEM 780 799 S3 OF REPEAT I1 (POTENTIAL).
FT TRANSMEM 806 825 S4 OF REPEAT I1 (POTENTIAL).
FT TRANSMEM 842 862 S5 OF REPEAT I1 (POTENTIAL).
FT TRANSMEM 914 939 S6 OF REPEAT I1 (POTENTIAL).
FT TRANSMEM 1201 1224 S1 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1238 1263 S2 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1270 1291 S3 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1296 1317 S4 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1337 1359 S5 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1444 1470 S6 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1524 1547 S1 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1559 1582 S2 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1589 1612 S3 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1623 1644 S4 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1660 1682 S5 OF REPEAT I11 (POTENTIAL).
FT TRANSMEM 1748 1772 S6 OF REPEAT I11 (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 548 548 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 592 592 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 740 740 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 803 803 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 841 841 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 864 864 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 946 946 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1365 1365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1374 1374 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1380 1380 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1388 1388 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1736 1736 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1774 1774 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1955 1955 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 558 558 H -> R.
FT VARIANT 1114 1114 /FTid=VAR 008955.
FT VARIANT 1404 1404 D -> N (IN LQT3).
FT VARIANT 1404 1404 /FTid=VAR 009935.
FT VARIANT 1404 1404 T -> M (IN LQT3).
FT VARIANT 1404 1404 /FTid=VAR 008956.
FT VARIANT 1404 1404 N -> S (IN LQT3).

Query Match 68.0%; Score 34; DB 1; Length 2016;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PSAAALTYSP 10
Db 1002 PSIAATPSP 1011
|||:|||||
|||:|||||

RESULT 17
PYRD_SULAC STANDARD; PRT; 291 AA.
AC 008958;
DT 15-DEC 1998 (Rel. 37, Created)
DT 16-OCT 2001 (Rel. 40, Last sequence update)
DT 15-JUN 2002 (Rel. 41, Last annotation update)
DE Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate oxidase)
DE (DHODase) (DHOD).
CN PYRD.
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31909 / NCBI 11770 / DSM 639;
RA Charlier D.R.M., Thia-Young T.L., Roovers M., Durbecq V., Legrain C.,
Glansdorff N.;

Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
-!- CATALYTIC ACTIVITY: (S)-dihydroorotate + O(2) -> orotate +
H(2)O(2).
-!- COFACTOR: FMN (BY SIMILARITY).
-!- PATHWAY: Pyrimidine biosynthesis; fourth step.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE DIHYDROOROTATE DEHYDROGENASE FAMILY.
SUBFAMILY 1.

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or send an email to license@isb-sib.ch).

EMBL; Y12823; CAA73354.1; ALT_INIT.
InterPro; IPR001295; DHO dh.
InterPro; IPR003009; FMN enzyme.
Pfam; PF01180; DHODase; 1.
TIGRfam; TIGR01037; PYRD subfam. 1.
PROSITE; PS00911; DHODASE_1; FALSE_NEG.
PROSITE; PS00912; DHODASE_2; 1.
Pyrimidine biosynthesis; Oxidoreductase; Flavoprotein; FMN.
FT NP BIND 224 232 FMN (POTENTIAL).
SQ SEQUENCE 291 AA; 31667 MW; 90C624D3BB0D30ED CRC64;

Query Match 67.0%; Score 33.5; DB 1; Length 291;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 PSAAALTYSP 10
Db 36 PSAITSKLTLYSP 48
|||:|||||
|||:|||||

RESULT 18
GBLP_SCHPO STANDARD; PRT; 314 AA.
AC Q10281; P78896;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Guanine nucleotide-binding protein beta subunit-like protein (Receptor
of activated protein kinase C).
CN RKP1 OR CPC2 OR SPAC6B12.15.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ED616;
RA Park S.-K., Yoo H.-S.;
RT "Molecular cloning and nucleotide sequence of Schizosaccharomycetes
pombe homologue of the receptor for activated protein kinase C gene.";
RL Korean J. Microbiol. 33:128-131(1995).
RN [2]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=ED616;
RX MEDLINE=21164691; PubMed=11263963;
RA Won M., Park S.-K., Hoe K.-L., Jang Y.-J., Chung K.-S., Kim D.-U.,
Kim H.-B., Yoo H.-S.;
RT "Rkp1/Cpc2, a fission yeast RACK1 homolog, is involved in actin
cytoskeleton organization through protein kinase C, Pck2, signaling.";
RL Biochem. Biophys. Res. Commun. 282:10-15(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;

```

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayles J., Baker S., Baeham D., Bowman S.,  
 RA Brooks K., Brown M., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Robben J., Gympre B.,  
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Burnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,  
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,  
 RA "The genome sequence of Schizosaccharomyces pombe."  
 Nature 415:871-880(2002).  
 [4]  
 RP SEQUENCE OF 5-314 FROM N.A.  
 RC STRAIN=PR745;  
 RX MEDLINE=98162722; PubMed=9501991;  
 RA Yoshioxa S., Kato K., Nakai K., Okayama H., Nojima H.;  
 RT "Identification of open reading frames in Schizosaccharomyces pombe  
 CDNA's";  
 RL DNA Res. 4:363-369(1997).  
 CC -1- FUNCTION: MAY BE A RECEPTOR FOR PROTEIN KINASE C IN THE REGULATION  
 OF ACTIN CYTOSKELETON ORGANIZATION DURING CELL WALL SYNTHESIS AND  
 MORPHOGENESIS.  
 CC -1- SUBUNIT: INTERACTS WITH PKC2.  
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH PARTICULATE FRACTIONS.  
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TREP-ASP DOMAINS).  
 CC -----  
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 CC -----  
 DR EMBL: L37885; AAA56865.2; -;  
 DR EMBL: AF320333; AAK38633.1; -;  
 DR EMBL: Z98531; CAB11079.1; -;  
 DR EMBL: D69247; BAA13908.1; -;  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 7.  
 DR PRINTS: PR00320; GPROTEINRPT.  
 DR ProDom: PD000018; WD40; 5.  
 DR SMART: SM00320; WD40; 7.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; 4.  
 DR PROSITE: PS00678; WD\_REPEATS\_2; 6.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 KW Repeat; WD repeat.  
 FT REPEAT 13 44 WD 1.  
 FT REPEAT 61 91 WD 2.  
 FT REPEAT 103 133 WD 3.  
 FT REPEAT 146 178 WD 4.  
 FT REPEAT 190 220 WD 5.  
 FT REPEAT 231 260 WD 6.  
 FT REPEAT 281 311 WD 7.  
 FT REPEAT 41 41 I -> L (IN REF. 1).  
 FT CONFLICT 41 41  
 SO SEQUENCE 314 AA; 34851 MW; 4B14707164E68ACD CRC64;  
 Query Match 66.0%; Score 33; DB 1; Length 314;

Best Local Similarity 50.0%; Pred. No. 29;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 PSAVALTSP 10  
 Db 284 PFCISLTWSP 293  
 RESULT 19  
 VMAV LPMV  
 ID VMAV LPMV STANDARD; PRT; 369 AA.  
 AC P27287;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DE 01-AUG-1992 (Rel. 23, Last annotation update)  
 DE Matrix protein.  
 GN M. M.  
 OS La Piedad-Michoacan-Mexico virus (LPMV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OC NCBI TaxID=11262;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91237338; PubMed=2033388;  
 RA Berg M., Sundqvist A., Moreno-Lopez J., Lime T.;  
 RT "Identification of the porcine paramyxovirus LPMV matrix protein  
 RT gene: comparative sequence analysis with other paramyxoviruses."  
 RL J. Gen. Virol. 72:1045-1050(1991).  
 CC -1- FUNCTION: THE M PROTEIN HAS A CRUCIAL ROLE IN VIRUS ASSEMBLY  
 CC AND INTERACTS WITH THE RNP COMPLEX AS WELL AS WITH THE VIRAL  
 CC MEMBRANE.  
 CC PIR: A38707; MFNZLA.  
 DR InterPro: IPR000982; Matrix.  
 DR Pfam: PF00661; Matrix; 1.  
 DR ProDom: PD000741; Matrix; 1.  
 KW Matrix protein; Envelope protein.  
 SQ SEQUENCE 369 AA; 41657 MW; B5362722PF8D6B5A CRC64;  
 Query Match 66.0%; Score 33; DB 1; Length 369;  
 Best Local Similarity 60.0%; Pred. No. 35;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 PSAVALTSP 10  
 Db 173 PFCISLTWSP 182  
 RESULT 20  
 ADHA UROHA  
 ID ADHA UROHA STANDARD; PRT; 375 AA.  
 AC P25405;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Alcohol dehydrogenase I-A (EC 1.1.1.1) (ADH IA).  
 OS Uromastix hardwickii (Indian spiny-tailed lizard).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Uromastixinae;  
 OC Uromastix.  
 NCBI TaxID=40250;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96195666; PubMed=8612630;  
 RA Hjeltnyist L., Shafiqat J., Siddiqi A.R., Oernvall H.;  
 RT "Linking of isozyme and class variability patterns in the emergence  
 RT of novel alcohol dehydrogenase functions. Characterization of  
 RT isozymes in Uromastix hardwickii.";  
 RL Eur. J. Biochem. 235:563-570(1996).  
 RN [2]  
 RP SEQUENCE OF 1-18.  
 RC TISSUE=Liver;  
 RX MEDLINE=92183888; PubMed=1544464;  
 RA Hjeltnyist L., Ericsson M., Shafiqat J., Carlquist M., Siddiqi A.R.,

RA Hookey J. O., Joernvall H.;  
 RT "Reptilian alcohol dehydrogenase. Heterogeneity relevant to class  
 RL multiplicity of the mammalian enzyme.";  
 CC FEBS Lett. 298:297-300(1992).  
 CC ! CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +  
 CC NADH.  
 CC ! COFACTOR: ZINC.  
 CC ! SUBUNIT: MULTIMERIC (WITH DIFFERENT RATIOS OF MONOMERS).  
 CC ! SUBCELLULAR LOCATION: Cytoplasmic.  
 CC ! MISCELLANEOUS: IN U.HARDWICKII THERE ARE TWO ISOZYMES OF ALCOHOL  
 CC DEHYDROGENASE I.  
 CC ! SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE  
 CC FAMILY.  
 CC PIR: S20429; S20429.  
 CC HSSP: P00427; ZOHX.  
 CC InterPro: IPR002328; ADH\_zinc.  
 CC InterPro: IPR002085; Adh\_zn\_family.  
 CC Pfam: PF00107; adh\_zinc; 1.  
 CC PROSITE: PS00559; ADH\_ZINC; 1.  
 CC (Oxidoreductase; Zinc; NAD; Multigene family; Acetylation.  
 FT MOD\_RES 1  
 FT METAL 46 46 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 67 67 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 97 97 ZINC (SECOND ATOM) (BY SIMILARITY).  
 FT METAL 100 100 ZINC (SECOND ATOM) (BY SIMILARITY).  
 FT METAL 103 103 ZINC (SECOND ATOM) (BY SIMILARITY).  
 FT METAL 111 111 ZINC (SECOND ATOM) (BY SIMILARITY).  
 FT METAL 174 174 ZINC (CATALYTIC) (BY SIMILARITY).  
 SQ SEQUENCE 475 AA; 39663 MW; F315BB77996D906 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 375;  
 Best Local Similarity 60.0%; Pred. No. 36;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSAVALTYSP 10  
 ||| :|||  
 Db :97 PSANETFSF 306

RESULT 21  
 VMAI SV41  
 ID VMAI SV41 STANDARD; PRT: 382 AA.  
 AC P25182;  
 DT 01 MAY-1992 (Rel. 22, Created)  
 DT 01 MAY 1992 (Rel. 22, Last sequence update)  
 DT 15-DEC 1998 (Rel. 37, Last annotation update)  
 DE Matrix protein.  
 GN M.  
 OS Simian virus 41 (SV41).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.  
 CC NCBI\_TaxID=11228;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Toshiiba/Chanock;  
 RX MEDLINE=91049440; PubMed=2173260;  
 RA Tsurudome M., Bando H., Nishio M., Iwamoto Y., Kawano M., Kondo K.,  
 RA Komada H., Ito Y.;  
 ET "Antigenic and structural properties of a paramyxovirus simian virus  
 RT 41 (SV41) reveal a close relationship with human parainfluenza type 2  
 RL virus.";  
 RL Virology 179:738-748(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Toshiiba/Chanock;  
 RX MEDLINE=91135794; PubMed=1651608;  
 RA Tsurudome M., Bando H., Kawano M., Matsumura H., Komada H., Nishio M.,  
 RA Ito Y.;  
 ET "Transfer of simian virus 41 (SV41) matrix gene are exclusively  
 RT dicistronic with the fusion gene which is also transcribed as a  
 RT monocistron.";  
 RL Virology 184:94-100(1991).  
 CC ! FUNCTION: THE M PROTEIN HAS A CRUCIAL ROLE IN VIRUS ASSEMBLY

CC AND INTERACTS WITH THE RNP COMPLEX AS WELL AS WITH THE VIRAL  
 CC MEMBRANE.  
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 CC EMBL: S48627; AAB19493.1; -  
 CC EMBL: X64275; CAA45566.1; -  
 CC EMBL: M62733; -; NOT\_ANNOTATED\_CDS.  
 CC PIR: A40563; MFNZ41.  
 CC InterPro: IPR000982; Matrix.  
 CC Pfam: PF00661; Matrix; 1.  
 CC ProDom: PD000741; Matrix; 1.  
 CC Matrix protein; Envelope protein.  
 KW Matrix protein; Envelope protein.  
 SQ SEQUENCE 382 AA; 42155 MW; B4C6DCE968E4A855 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 382;  
 Best Local Similarity 60.0%; Pred. No. 36;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSAVALTYSP 10  
 ||| :|||  
 Db 170 PTFVSLTYCP 179

RESULT 22  
 EFIA DESMO  
 ID EFIA DESMO STANDARD; PRT: 438 AA.  
 AC P41203;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF Tu).  
 GN TUF OR TUX.  
 OS Desulfurococcus mobilis.  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;  
 OC Desulfurococcaceae; Desulfurococcus.  
 CC NCBI\_TaxID=2274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 2126;  
 RX MEDLINE=95206243; PubMed=7898436;  
 RA Ceccarelli E., Bocchetta M., Creti R., Sanangelantoni A.M., Tiboni O.,  
 RA Cammarano F.;  
 ET "Chromosomal organization and nucleotide sequence of the genes for  
 RT elongation factors EF-1 alpha and EF-2 and ribosomal proteins S7 and  
 RT S10 of the hyperthermophilic archaeum Desulfurococcus mobilis.";  
 RL Mol. Gen. Genet. 246:687-696(1995).  
 CC !- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
 CC AMINOACYL-tRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
 CC BIOSYNTHESIS.  
 CC !- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC !- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC EF-TU/EF-1A SUBFAMILY.  
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 CC EMBL: X73582; CAA51984.1; -  
 CC HSSP: P07157; IAIP.  
 CC InterPro: IPR004539; EFl\_alpha.  
 CC InterPro: IPR004160; EFTU\_Cterm.  
 CC InterPro: IPR004161; EFTU\_D2.

DR InterPro: IPR000795; EF\_GTPbind.  
 DR Pfam: PF00009; GTP\_EFTU; 1.  
 DR Pfam: PF03143; GTP\_EFTU\_D3; 1.  
 DR Pfam: PF03144; GTP\_EFTU\_D2; 1.  
 DR PRINTS: PRO0315; ELONGATNFACT.  
 DR TIGRfam: TIGR00483; EF-1\_alpha; 1.  
 DR PROSITE: PS0301; EFATOR\_GTP; 1.  
 DR Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NP\_BIND 15 22 GTP (BY SIMILARITY).  
 FT NP\_BIND 92 96 GTP (BY SIMILARITY).  
 FT NP\_BIND 154 157 GTP (BY SIMILARITY).  
 SQ SEQUENCE 438 AA; 46737 MW; 4A4955EB6CB39427 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 438;  
 Best Local Similarity 50.0%; Pred. No. 42;  
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10  
 DB 338 PTAIAVGYTP 347

RESULT 23  
 FIBI\_ADE40 STANDARD; PRT; 547 AA.  
 P18047;  
 01-NOV-1990 (Rel. 16, Created)  
 01-NOV-1990 (Rel. 16, Last sequence update)  
 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Fiber protein 1.  
 OS Human adenovirus type 40.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=28284;  
 RN [1]\_TaxID=28284;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=89370295; PubMed=2773314;  
 RX Kidd A.H.; Erasmus M.J.;  
 RT "Sequence characterization of the adenovirus 40 fiber gene."  
 VL Virology 172:134-144(1989).  
 CC - FUNCTION: RECOGNIZES THE CELL RECEPTOR; SERVES AS THE LIGAND  
 BETWEEN THE ADENOVIRUS CAPSID AND THE HOST CELL RECEPTOR.  
 CC - SUBUNIT: HOMOTRIMER.

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DR EMBL: M28822; AAA03234.1; -;  
 DR EMBL: L19443; AAC13980.1; -;  
 DR PIR: B30336; ERADF4.  
 DR HSSP: P1818; 1XNB.  
 DR InterPro: IPR000939; Adeno\_fiber2.  
 DR InterPro: IPR000978; Adeno\_fiber\_knob.  
 DR InterPro: IPR000931; Adeno\_fiber.  
 DR Pfam: PF00541; adeno\_fiber; 1.  
 DR Pfam: PF00608; adeno\_fiber2; 9.  
 DR PRINTS: PRO0307; ADENOVSFIBRE.  
 KM Fiber protein.  
 SQ SEQUENCE 547 AA; 59113 MW; D1DDC36C4C935DE1 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 547;  
 Best Local Similarity 87.5%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AVALTYSP 10  
 DB 201 AVALKYSP 208

RESULT 24  
 ID ATKA ANASL STANDARD; PRT; 561 AA.  
 AC O9REX2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium-transporting ATPase A chain (EC 3.6.3.12) (Potassium-  
 DE translocating ATPase A chain) (ATP phosphohydrolase [potassium-  
 DE transporting] A chain) (Potassium binding and translocating subunit  
 DE A).  
 GN KdPA.  
 OS Anabaena sp. (strain L31).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
 OX NCBI\_TaxID=29412;  
 RN [1]\_TaxID=29412;  
 RP SEQUENCE FROM N.A.  
 RA Ballal A.D.; Gassel M.; Schlessinger E.; Rajaram H.; Apté S.K.;  
 RA Altendorf K.;  
 RT "The kdp operon of the heterocystous nitrogen-fixing cyanobacterium  
 RT Anabaena sp. strain L-31."  
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: ONE OF THE COMPONENTS OF THE HIGH-AFFINITY ATP-DRIVEN  
 CC POTASSIUM TRANSPORT (OR KDP) SYSTEM, WHICH CATALYZES THE  
 CC HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF HYDROGEN AND  
 CC POTASSIUM IONS (BY SIMILARITY).  
 CC - CATALYTIC ACTIVITY: ATP + H(2)O + K(+) (Out) = ADP + phosphate +  
 CC K(+) (In).  
 CC - SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (Probable).  
 CC - SIMILARITY: BELONGS TO THE KdPA FAMILY.

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DR EMBL: AF213466; AAF19986.1; -;  
 DR InterPro: IPR004623; K\_ATPaseA.  
 DR TIGRfam: TIGR00680; kdpA; 1.  
 KM Hydrolyase; Transport; Potassium transpore; Transmembrane;  
 KW Inner membrane.  
 FT TRANSMEM 2 22 POTENTIAL.  
 FT TRANSMEM 65 85 POTENTIAL.  
 FT TRANSMEM 135 155 POTENTIAL.  
 FT TRANSMEM 177 197 POTENTIAL.  
 FT TRANSMEM 253 273 POTENTIAL.  
 FT TRANSMEM 280 300 POTENTIAL.  
 FT TRANSMEM 327 347 POTENTIAL.  
 FT TRANSMEM 353 373 POTENTIAL.  
 FT TRANSMEM 378 398 POTENTIAL.  
 FT TRANSMEM 413 433 POTENTIAL.  
 FT TRANSMEM 482 502 POTENTIAL.  
 FT TRANSMEM 532 552 POTENTIAL.  
 SQ SEQUENCE 561 AA; 60776 MW; C8EE833F0E07D81 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 561;  
 Best Local Similarity 75.0%; Pred. No. 55;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 8  
 DB 430 PSAAVATYSP 437

RESULT 25  
 ID PTSA STRMU STANDARD; PRT; 664 AA.  
 AC P12655;  
 DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DE PTS system, sucrose-specific IIAC component (EIABC-SCR) (Sucrose-  
DE permease IIAC component) (Phosphotransferase enzyme II, ABC  
DE component) (EC 2.7.1.69) (EII-SCR).  
GN SCRA.  
OS Streptococcus mutans.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
CX NCBI TaxID:1109;  
RN [1]  
RV SEQUENCE FROM N.A.  
RC STRAIN-GS-5;  
RX MEDLINE=9121027; PubMed=2536656;  
RA Sato Y., Poy F., Jacobson G.R., Kuramitsu H.K.;  
RT "Characterization and sequence analysis of the scrA gene encoding  
RT enzyme IIScr of the Streptococcus mutans  
RT phosphoenolpyruvate-dependent sucrose phosphotransferase system.";  
RL J. Bacteriol. 171:263-271(1989).  
RN [2]  
RN SEQUENCE OF 639-664 FROM N.A.  
RP STRAIN-GS-5;  
RX MEDLINE=9129360; PubMed=8336109;  
RA Sato Y., Yamamoto Y., Kizaki H., Kuramitsu H.K.;  
RT "Isolation, characterization and sequence analysis of the scrK gene  
RT encoding fructokinase of Streptococcus mutans.";  
RL J. Gen. Microbiol. 139:921-927(1993).  
CC [1] FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT  
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS). A MAJOR CARBOHYDRATE ACTIVE  
CC -TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE  
CC AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY  
CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS  
CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO  
CC THE SUGAR.  
CC [1] CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein  
CC histidine + sugar phosphate.  
CC [1] SUBCELLULAR LOCATION: Integral membrane protein.  
CC [1] SIMILARITY: CONTAINS 1 PTS\_EIIA DOMAIN.  
CC [1] SIMILARITY: CONTAINS 1 PTS\_EIIB DOMAIN.  
CC [1] SIMILARITY: CONTAINS 1 PTS\_EIIC DOMAIN.  
CC [1] SIMILARITY: CONTAINS 1 PTS\_EIIB DOMAIN.  
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CC -----  
DR EMBL; M22711; AAA26971.1; -;  
DR EMBL; D13175; BAA02466.1; -;  
DR PIR; B32243; B32243.  
DR HSSP; FOR837; 1GLC.  
DR InterPro; IPR001127; PTS\_EIIA.  
DR InterPro; IPR001996; PTS\_EIIB.  
DR InterPro; IPR003352; PTS\_EIIC.  
DR Pfam; PF00358; PTS\_EIIA\_1; 1.  
DR Pfam; PF00367; PTS\_EIIB\_1.  
DR Pfam; PF02378; PTS\_EIIC\_1.  
DR ProDom; PRO01476; PTS\_EIIB\_1.  
DR ProDom; PRO02243; PTS\_EIIA\_1.  
DR TIGRFAMs; TIGR00826; EIIB\_1.  
DR TIGRFAMs; TIGR00830; PTBA; 1.  
DR PROSITE; PS00371; PTS\_EIIA\_1; 1.  
DR PROSITE; PS01035; PTS\_EIIB\_CYS; 1.  
DR Phosphotransferase system; Sugar transport; Transferase;  
KW Phosphorylation; Transmembrane.  
FT DOMAIN 1 40 EIIB DOMAIN.  
FT DOMAIN ? ? EIIIC DOMAIN.  
FT DOMAIN 533 664 EIIA DOMAIN.  
FT MOD\_RES 25 25 PHOSPHORYLATION (BY SIMILARITY).  
FT MOD\_RES 331 331 PHOSPHORYLATION (BY SIMILARITY).  
FT MOD\_RES 545 545 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 664 AA; 69988 MW; 809E63E3281A9A1 CRC64;  
Query Match 66.0%; Score 33; DB 1; Length 664;  
Best Local Similarity 60.0%; Pred. No. 67;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 PSVAALTYSP 10  
Db 264 PSAVDFTFTP 273

Search completed: January 3, 2003, 13:02:00  
Job time : 5.69565 secs